

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/882,774A
Source: IFW/6
Date Processed by STIC: 9/23/05

ENTERED



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/882,774A

DATE: 09/23/2005
TIME: 17:02:01

Input Set : A:\003592-007 ST25.txt
Output Set: N:\CRF4\09232005\I882774A.raw

4 <110> APPLICANT: Houston, Michael E.
5 Hedges, Robert
7 <120> TITLE OF INVENTION: Use of Coiled-Coil Structural Scaffold to Generate
8 Structure-Specific Peptides
10 <130> FILE REFERENCE: 003592-007
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/882,774A
C--> 12 <141> CURRENT FILING DATE: 2001-06-14
12 <150> PRIOR APPLICATION NUMBER: US 60/211,892
13 <151> PRIOR FILING DATE: 2000-06-14
15 <150> PRIOR APPLICATION NUMBER: US 60/213,387
16 <151> PRIOR FILING DATE: 2000-06-23
18 <160> NUMBER OF SEQ ID NOS: 17
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 619
24 <212> TYPE: PRT
25 <213> ORGANISM: Streptococcus pneumoniae
27 <400> SEQUENCE: 1
29 Met Asn Lys Lys Lys Met Ile Leu Thr Ser Leu Ala Ser Val Ala Ile
30 1 5 10 15
32 Leu Gly Ala Gly Phe Val Ala Ser Gln Pro Thr Val Val Arg Ala Glu
33 20 25 30
35 Glu Ser Pro Val Ala Ser Gln Ser Lys Ala Glu Lys Asp Tyr Asp Ala
36 35 40 45
38 Ala Lys Lys Asp Ala Lys Asn Ala Lys Lys Ala Val Glu Asp Ala Gln
39 50 55 60
41 Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu Asp
42 65 70 75 80
44 Gln Lys Lys Thr Glu Glu Lys Ala Ala Leu Glu Lys Ala Ala Ser Glu
45 85 90 95
47 Glu Met Asp Lys Ala Val Ala Ala Val Gln Gln Ala Tyr Leu Ala Tyr
48 100 105 110
50 Gln Gln Ala Thr Asp Lys Ala Ala Lys Asp Ala Ala Asp Lys Met Ile
51 115 120 125
53 Asp Glu Ala Lys Lys Arg Glu Glu Glu Ala Lys Thr Lys Phe Asn Thr
54 130 135 140
56 Val Arg Ala Met Val Val Pro Glu Pro Glu Gln Leu Ala Glu Thr Lys
57 145 150 155 160
59 Lys Lys Ser Glu Glu Ala Lys Gln Lys Ala Pro Glu Leu Thr Lys Lys
60 165 170 175
62 Leu Glu Glu Ala Lys Ala Lys Leu Glu Glu Ala Glu Lys Lys Ala Thr
63 180 185 190
65 Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Val Ala Pro Gln Ala Lys

Q6

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66	195	200	205
68	Ile Ala Glu Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu Lys		
69	210	215	220
71	Glu Ile Asp Glu Ser Glu Ser Glu Asp Tyr Ala Lys Glu Gly Phe Arg		
72	225	230	235
74	240		
74	Ala Pro Leu Gln Ser Lys Leu Asp Ala Lys Lys Ala Lys Leu Ser Lys		
75	245	250	255
77	Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala Glu Ile Ala		
78	260	265	270
80	Lys Leu Glu Asp Gln Leu Lys Ala Ala Glu Glu Asn Asn Asn Val Glu		
81	275	280	285
83	Asp Tyr Phe Lys Glu Gly Leu Glu Lys Thr Ile Ala Ala Lys Lys Ala		
84	290	295	300
86	Glu Leu Glu Lys Thr Glu Ala Asp Leu Lys Lys Ala Val Asn Glu Pro		
87	305	310	315
89	320		
89	Glu Lys Pro Ala Pro Ala Pro Glu Thr Pro Ala Pro Glu Ala Pro Ala		
90	325	330	335
92	Glu Gln Pro Lys Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro Lys		
93	340	345	350
95	Pro Glu Lys Pro Ala Glu Gln Pro Lys Pro Glu Lys Thr Asp Asp Gln		
96	355	360	365
98	Gln Ala Glu Glu Asp Tyr Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg		
99	370	375	380
101	Leu Thr Gln Gln Gln Pro Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro		
102	385	390	395
104	400		
104	Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr		
105	405	410	415
107	Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp Tyr		
108	420	425	430
110	Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn		
111	435	440	445
113	Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp		
114	450	455	460
116	Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met		
117	465	470	475
119	480		
119	Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala		
120	485	490	495
122	Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr		
123	500	505	510
125	Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn		
126	515	520	525
128	Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp		
129	530	535	540
131	Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met		
132	545	550	555
134	560		
134	Ala Thr Gly Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala		
135	565	570	575
137	Ser Gly Ala Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp		
138	580	585	590

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140 Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala Val Asn Thr Thr Val Asp
 141 595 600 605
 143 Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp Val
 144 610 615
 147 <210> SEQ ID NO: 2
 148 <211> LENGTH: 40
 149 <212> TYPE: PRT
 150 <213> ORGANISM: Artificial Sequence
 152 <220> FEATURE:
 153 <223> OTHER INFORMATION: stabilizing strand
 155 <220> FEATURE:
 156 <221> NAME/KEY: MOD_RES
 157 <222> LOCATION: (2)
 158 <223> OTHER INFORMATION: Nle
 160 <400> SEQUENCE: 2
 W--> 162 Cys Xaa Gly Gly Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala
 163 1 5 10 15
 165 Leu Lys Lys Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala Leu Lys
 166 20 25 30
 168 Lys Glu Ile Glu Ala Leu Lys Lys
 169 35 40
 171 <210> SEQ ID NO: 3
 172 <211> LENGTH: 38
 173 <212> TYPE: PRT
 174 <213> ORGANISM: Artificial Sequence
 176 <220> FEATURE:
 177 <223> OTHER INFORMATION: hybrid sequence
 179 <220> FEATURE:
 180 <221> NAME/KEY: MOD_RES
 181 <222> LOCATION: (2)
 182 <223> OTHER INFORMATION: Nle
 184 <400> SEQUENCE: 3
 W--> 186 Cys Xaa Gly Ile Glu Glu Leu Glu Lys Lys Ile Thr Glu Leu Lys Gln
 187 1 5 10 15
 189 Lys Ile Asp Ala Leu Glu Asn Gln Ile His Arg Leu Glu Gln Glu Ile
 190 20 25 30
 192 Lys Glu Leu Asp Glu Ser
 193 35
 195 <210> SEQ ID NO: 4
 196 <211> LENGTH: 38
 197 <212> TYPE: PRT
 198 <213> ORGANISM: Artificial Sequence
 200 <220> FEATURE:
 201 <223> OTHER INFORMATION: hybrid sequence
 203 <220> FEATURE:
 204 <221> NAME/KEY: MOD_RES
 205 <222> LOCATION: (2)
 206 <223> OTHER INFORMATION: Nle
 208 <400> SEQUENCE: 4

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W--> 210 Cys Xaa Gly Leu Glu Glu Ala Glu Lys Lys Ala Thr Glu Ala Lys Gln
 211 1 5 10 15
 213 Lys Val Asp Ala Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu
 214 20 25 30
 216 Lys Glu Ile Asp Glu Ser
 217 35
 219 <210> SEQ ID NO: 5
 220 <211> LENGTH: 20
 221 <212> TYPE: PRT
 222 <213> ORGANISM: Artificial Sequence
 224 <220> FEATURE:
 225 <223> OTHER INFORMATION: consensus sequence
 227 <220> FEATURE:
 228 <221> NAME/KEY: PEPTIDE
 229 <222> LOCATION: (4)..(20)
 230 <223> OTHER INFORMATION: Amino acids 4, 5, 12, 16 and 20 are Xaa wherein Xaa = any
 amino acid
 231 acid
 233 <400> SEQUENCE: 5

W--> 235 Glu Glu Leu Xaa Xaa Lys Ile Asp Glu Leu Asp Xaa Glu Ile Ala Xaa
 236 1 5 10 15
 238 Leu Glu Lys Xaa
 239 20
 241 <210> SEQ ID NO: 6
 242 <211> LENGTH: 8
 243 <212> TYPE: PRT
 244 <213> ORGANISM: Artificial Sequence
 246 <220> FEATURE:
 247 <223> OTHER INFORMATION: consensus sequence
 249 <400> SEQUENCE: 6
 251 Glu Glu Leu Ser Asp Lys Ile Asp
 252 1 5
 254 <210> SEQ ID NO: 7
 255 <211> LENGTH: 27
 256 <212> TYPE: PRT
 257 <213> ORGANISM: Artificial Sequence
 259 <220> FEATURE:
 260 <223> OTHER INFORMATION: hybrid sequence
 262 <220> FEATURE:
 263 <221> NAME/KEY: MOD_RES
 264 <222> LOCATION: (2)
 265 <223> OTHER INFORMATION: Nle
 267 <400> SEQUENCE: 7

W--> 269 Cys Xaa Gly Glu Ile Glu Ala Leu Lys Lys Ile Glu Glu Leu Ser
 270 1 5 10 15
 272 Asp Lys Ile Asp Glu Leu Glu Lys Glu Ile Lys
 273 20 25
 275 <210> SEQ ID NO: 8
 276 <211> LENGTH: 21
 277 <212> TYPE: PRT

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Input Set : A:\003592-007 ST25.txt
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278 <213> ORGANISM: Haemophilus influenzae
280 <400> SEQUENCE: 8
282 Ile Lys Lys Val Leu Glu Ile Gly Leu Asn Met Ser Gln Glu Ala Ser
283 1 5 10 15
285 Asn Leu Thr Ser Ala
286 20
288 <210> SEQ ID NO: 9
289 <211> LENGTH: 27
290 <212> TYPE: PRT
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: hybrid sequence
296 <400> SEQUENCE: 9
298 Glu Ala Glu Ile Lys Lys Leu Leu Glu Ile Ile Leu Asn Leu Ser Gln
299 1 5 10 15
301 Glu Ile Ser Asn Leu Thr Ser Ala Leu Lys Gly
302 20 25
304 <210> SEQ ID NO: 10
305 <211> LENGTH: 20
306 <212> TYPE: PRT
307 <213> ORGANISM: Streptococcus pneumoniae
309 <400> SEQUENCE: 10
311 Leu Glu Lys Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Gln Ala
312 1 5 10 15
314 Glu Gln Val Leu
315 20
317 <210> SEQ ID NO: 11
318 <211> LENGTH: 15
319 <212> TYPE: PRT
320 <213> ORGANISM: Streptococcus pneumoniae
322 <400> SEQUENCE: 11
324 Leu Glu Asp Asn Leu Lys Asp Ala Glu Thr Asn Asn Val Glu Asp
325 1 5 10 15
327 <210> SEQ ID NO: 12
328 <211> LENGTH: 10
329 <212> TYPE: PRT
330 <213> ORGANISM: Streptococcus pneumoniae
332 <400> SEQUENCE: 12
334 Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys
335 1 5 10
337 <210> SEQ ID NO: 13
338 <211> LENGTH: 35
339 <212> TYPE: PRT
340 <213> ORGANISM: Artificial Sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: hybrid sequence
345 <400> SEQUENCE: 13
347 Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Leu Glu Asp Asn Leu
348 1 5 10 15

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 2
Seq#:3; Xaa Pos. 2
Seq#:4; Xaa Pos. 2
Seq#:5; Xaa Pos. 4, 5, 12, 16, 20
Seq#:7; Xaa Pos. 2
Seq#:15; Xaa Pos. 1, 2, 3, 4, 5, 6, 7
Seq#:16; Xaa Pos. 2, 5, 6, 8, 9, 10

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0